

- 1 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chicheportiche, Yves
Browning, Jeffrey L.
- (ii) TITLE OF INVENTION: A TUMOR NECROSIS FACTOR RELATED LIGAND
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BIOGEN, INC.
 - (B) STREET: 14 CAMBRIDGE CENTER
 - (C) CITY: CAMBRIDGE
 - (D) STATE: MA
 - (E) COUNTRY: US
 - (F) ZIP: 02142
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: not yet assigned
 - (B) FILING DATE: 07-May-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: FLYNN, KERRY A.
 - (B) REGISTRATION NUMBER: 33,693
 - (C) REFERENCE/DOCKET NUMBER: A003 PCT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 679-3583
 - (B) TELEFAX: (617) 679-2838

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

-2-

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: TNF family related protein

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G GTG CTG AGC CTG GGC CTG GCG CTG GCC TGC CTT GGC CTC CTG CTG	46
Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu	
1 5 10 15	
GTC GTG GTC AGC CTG GGG AGC TGG GCA ACG CTG TCT GCC CAG GAG CCT	94
Val Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro	
20 25 30	
TCT CAG GAG GAG CTG ACA GCA GAG GAC CGC CGG GAG CCC CCT GAA CTG	142
Ser Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu	
35 40 45	
AAT CCC CAG ACA GAG GAA AGC CAG GAT GTG GTA CCT TTC TTG GAA CAA	190
Asn Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln	
50 55 60	
CTA GTC CGG CCT CGA AGA AGT GCT CCT AAA GGC CGG AAG GCG CGG CCT	238
Leu Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro	
65 70 75	
CGC CGA GCT ATT GCA GCC CAT TAT GAG GTT CAT CCT CGG CCA GGA CAG	286
Arg Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln	
80 85 90 95	
GAT GGA GCA CAA GCA GGT GTG GAT GGG ACA GTG AGT GGC TGG GAA GAG	334
Asp Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu	
100 105 110	
ACC AAA ATC AAC AGC TCC AGC CCT CTG CGC TAC GAC CGC CAG ATT GGG	382
Thr Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly	
115 120 125	
GAA TTT ACA GTC ATC AGG GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG	430
Glu Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val	
130 135 140	

-3-

CAC TTT GAT GAG GGA AAG GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG	478
His Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val	
145 150 155	
AAC GGT GTG CTG GCC CTG CGC TGC CTG GAA GAA TTC TCA GCC ACA GCA	526
Asn Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala	
160 165 170 175	
GCA AGC TCT CCT GGG CCC CAG CTC CGT TTG TGC CAG GTG TCT GGG CTG	574
Ala Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu	
180 185 190	
TTG CCG CTG CGG CCA GGG TCT TCC CTT CGG ATC CGC ACC CTC CCC TGG	622
Leu Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp	
195 200 205	
GCT CAT CTT AAG GCT GCC CCC TTC CTA ACC TAC TTT GGA CTC TTT CAA	670
Ala His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln	
210 215 220	
GTT CAC TGAGGGGCCT TGCTCTCCCA GATTCCTTAA ACTTTCCTG GCTCCAGGAG	726
Val His	
225	
CATCACCACA CCTCCCTACC CCACCCCCAC TCCTCCACCC CCTCGCTGCT CCTTGGTCCA	786
GTCCTGTCTC TCCTCAAAGG CAGCCAGAGC TTGTTACAT GTTTCATT CACAGACGTA	846
TCCTTGCTCT TCTTAACATC CCATCCCACC ACAACTATCC ACCTCACTAG CTCCCAAAGC	906
CCCTACTTAT CCCTGACTCC CCCACCCACT CACCCGACCA CGTGTTTATT GACTTTGTGC	966
ACCAGGCACT GAGATGGGCT GGACCTGGTG GCAGGAAGCC AGAGAACCTG GGACTAGGCC	1026
AGAAGTTCCC AACTGTGAGG GGGAAGAGCT GGGGACAAGC TCCTCCCTGG ATCCCTGTGG	1086
ATTTTGAAAA GATACTATTT TTATTATTAT TGTGACAAAA TGTTAAATGG ATATTAAAGA	1146
GAATAAATCA TGATTTCTCT TC	1168

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

-4-

Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Val
 1 5 10 15
 Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro Ser
 20 25 30
 Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu Asn
 35 40 45
 Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln Leu
 50 55 60
 Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro Arg
 65 70 75 80
 Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
 85 90 95
 Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Thr
 100 105 110
 Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly Glu
 115 120 125
 Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
 130 135 140
 Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asn
 145 150 155 160
 Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
 165 170 175
 Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
 180 185 190
 Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
 195 200 205
 His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
 210 215 220
 His
 225

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1373 base pairs
 (B) TYPE: nucleic acid

-5-

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: TNF family related protein

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCA TTG TTA GAC TTT GAA ATT TCC GCC CGC CGG CTC CCC CTC CCC	48
Met Ser Leu Leu Asp Phe Glu Ile Ser Ala Arg Arg Leu Pro Leu Pro	
1 5 10 15	
CGA TCC CTC GGG TCC CGG GAT GGG GGG GCG GTG AGG CAG GCA CAG CCC	96
Arg Ser Leu Gly Ser Arg Asp Gly Gly Ala Val Arg Gln Ala Gln Pro	
20 25 30	
CCC GCC CCC ATG GCC GCC CGT CGG AGC CAG AGG CGG AGG GGG CGC CGG	144
Pro Ala Pro Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg	
35 40 45	
GGG GAG CCG GGC ACC GCC CTG CTG GTC CCG CTC GCG CTG GGC CTG GGC	192
Gly Glu Pro Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly	
50 55 60	
CTG GCG CTG GCC TGC CTC GGC CTC CTG CTG GCC GTG GTC AGT TTG GGG	240
Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly	
65 70 75 80	
AGC CGG GCA TCG CTG TCC GCC CAG GAG CCT GCC CAG GAG GAG CTG GTG	288
Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val	
85 90 95	
GCA GAG GAG GAC CAG GAC CCG TCG GAA CTG AAT CCC CAG ACA GAA GAA	336
Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu	
100 105 110	
AGC CAG GAT CCT GCG CCT TTC CTG AAC CGA CTA GTT CGG CCT CGC AGA	384
Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg	
115 120 125	

-6-

AGT GCA CCT AAA GGC CGG AAA ACA CGG GCT CGA AGA GCG ATC GCA GCC	432
Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala	
130 135 140	
CAT TAT GAA GTT CAT CCA CGA CCT GGA CAG GAC GGA GCG CAG GCA GGT	480
His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly	
145 150 155 160	
GTG GAC GGG ACA GTG AGT GGC TGG GAG GAA GCC AGA ATC AAC AGC TCC	528
Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser	
165 170 175	
AGC CCT CTG CGC TAC AAC CGC CAG ATC GGG GAG TTT ATA GTC ACC CGG	576
Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg	
180 185 190	
GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG CAC TTT GAT GAG GGG AAG	624
Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys	
195 200 205	
GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG GAT GGT GTG CTG GCC CTG	672
Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu	
210 215 220	
CGC TGC CTG GAG GAA TTC TCA GCC ACT GCG GCC AGT TCC CTC GGG CCC	720
Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro	
225 230 235 240	
CAG CTC CGC CTC TGC CAG GTG TCT GGG CTG TTG GCC CTG CGG CCA GGG	768
Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly	
245 250 255	
TCC TCC CTG CGG ATC CGC ACC CTC CCC TGG GCC CAT CTC AAG GCT GCC	816
Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala	
260 265 270	
CCC TTC CTC ACC TAC TTC GGA CTC TTC CAG GTT CAC TGAGGGGCCC	862
Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His	
275 280	
TGGTCTCCCC ACAGTCGTCC CAGGCTGCCG GCTCCCCTCG ACAGCTCTCT GGGCACCCGG	922
TCCCCCTCTGC CCCACCCTCA GCCGCTCTTT GCTCCAGACC TGCCCCCTCCC TCTAGAGGCT	982
GCCTGGGCCT GTTCACGTGT TTTCCATCCC ACATAAATAC AGTATTCCCA CTCTTATCTT	1042
ACAACTCCCC CACCGCCCCAC TCTCCACCTC ACTAGCTCCC CAATCCCTGA CCCTTTGAGG	1102
CCCCCAGTGA TCTCGACTCC CCCCTGGCCA CAGACCCCCA GGGCATTGTG TTCACTGTAC	1162
TCTGTGGGCA AGGATGGGTC CAGAAGACCC CACTTCAGGC ACTAAGAGGG GCTGGACCTG	1222

-7-

GCGGCAGGAA GCCAAAGAGA CTGGGCCTAG GCCAGGAGTT CCCAAATGTG AGGGGCGAGA 1282
 AACAAAGACAA GCTCCTCCCT TGAGAATTCC CTGTGGATTT TTAAACAGA TATTATTTTT 1342
 ATTATTATTG TGACAAAATG TTGATAAATG G 1373

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Leu	Leu	Asp	Phe	Glu	Ile	Ser	Ala	Arg	Arg	Leu	Pro	Leu	Pro	1	5	10	15
Arg	Ser	Leu	Gly	Ser	Arg	Asp	Gly	Gly	Ala	Val	Arg	Gln	Ala	Gln	Pro	20	25	30	
Pro	Ala	Pro	Met	Ala	Ala	Arg	Arg	Ser	Gln	Arg	Arg	Arg	Gly	Arg	Arg	35	40	45	
Gly	Glu	Pro	Gly	Thr	Ala	Leu	Leu	Val	Pro	Leu	Ala	Leu	Gly	Leu	Gly	50	55	60	
Leu	Ala	Leu	Ala	Cys	Leu	Gly	Leu	Leu	Leu	Ala	Val	Val	Ser	Leu	Gly	65	70	75	80
Ser	Arg	Ala	Ser	Leu	Ser	Ala	Gln	Glu	Pro	Ala	Gln	Glu	Glu	Leu	Val	85	90	95	
Ala	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Glu	Leu	Asn	Pro	Gln	Thr	Glu	Glu	100	105	110	
Ser	Gln	Asp	Pro	Ala	Pro	Phe	Leu	Asn	Arg	Leu	Val	Arg	Pro	Arg	Arg	115	120	125	
Ser	Ala	Pro	Lys	Gly	Arg	Lys	Thr	Arg	Ala	Arg	Arg	Ala	Ile	Ala	Ala	130	135	140	
His	Tyr	Glu	Val	His	Pro	Arg	Pro	Gly	Gln	Asp	Gly	Ala	Gln	Ala	Gly	145	150	155	160
Val	Asp	Gly	Thr	Val	Ser	Gly	Trp	Glu	Glu	Ala	Arg	Ile	Asn	Ser	Ser	165	170	175	

-8-

Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg
180 185 190

Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys
195 200 205

Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu
210 215 220

Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro
225 230 235 240

Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly
245 250 255

Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala
260 265 270

Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His
275 280